RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: _10/521,478A_

Source: _1FwO_

Date Processed by STIC: _8/31/06_

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RAW SEQUENCE LISTING   DATE: 08/31/2006
PATENT APPLICATION: US/10/521,478A   TIME: 09:06:41

Input Set : **N:\RJAVED\10521478.txt**
Output Set: **N:\CRF4\08312006\J521478A.raw**

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   4 <110> APPLICANT: Michel, Albrecht
   5         Scheffler, Brian E.
   6         Netherland, Michael D.
   7         Dayan, Franck E.
   8         Arias de Ares, Renee S.
  10 <120> TITLE OF INVENTION: HERBICIDE-RESISTANT PLANTS, AND POLYNUCLEOTIDES AND
  11       METHODS FOR PROVIDING SAME
W--> 13 <130> FILE REFERENCE:
C--> 15 <140> CURRENT APPLICATION NUMBER: US/10/521,478A
C--> 16 <141> CURRENT FILING DATE: 2005-01-17
  18 <160> NUMBER OF SEQ ID NOS: 8
  20 <170> SOFTWARE: PatentIn Ver. 2.1
  22 <210> SEQ ID NO: 1
  23 <211> LENGTH: 1982
  24 <212> TYPE: DNA
  25 <213> ORGANISM: Hydrilla verticillata
  27 <220> FEATURE:
  28 <221> NAME/KEY: CDS
  29 <222> LOCATION: (6)..(1748)
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  37 Leu Gln Asn Arg Tyr Pro Ala Ser Ser Ser Val Ser Cys Phe Leu Gly
  38                  20                  25                  30
  40 aaa gag tac aga tgc aac agt atg tta gga ttc tgc ggt agt gga aaa  146
  41 Lys Glu Tyr Arg Cys Asn Ser Met Leu Gly Phe Cys Gly Ser Gly Lys
  42              35                  40                  45
  44 ttg gct ttt ggc gca aat gca ccc tat tct aag att gca gct acc aaa  194
  45 Leu Ala Phe Gly Ala Asn Ala Pro Tyr Ser Lys Ile Ala Ala Thr Lys
  46          50                  55                  60
  48 cca aag ccc aaa ctt cgc cct ttg aag gtc aac tgc atg gat ttc cca  242
  49 Pro Lys Pro Lys Leu Arg Pro Leu Lys Val Asn Cys Met Asp Phe Pro
  50      65                  70                  75
  52 aga cct gat ata gat aac act gct aat ttc ttg gaa gct gct gct ctt  290
  53 Arg Pro Asp Ile Asp Asn Thr Ala Asn Phe Leu Glu Ala Ala Ala Leu
  54  80                  85                  90                  95
  56 tct tcc tct ttt cgc aat tca gca aga cca agt aaa cct ctt caa gtt  338
  57 Ser Ser Ser Phe Arg Asn Ser Ala Arg Pro Ser Lys Pro Leu Gln Val
  58              100                 105                 110
  60 gta att gct ggt gca ggt ttg gct ggt ctt tca aca gca aag tat ctc  386
  61 Val Ile Ala Gly Ala Gly Leu Ala Gly Leu Ser Thr Ala Lys Tyr Leu
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Input Set : N:\RJAVED\10521478.txt
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64 gca gat gca ggg cac ata ccc ata cta ctg gag gct aga gat gta ttg    434
65 Ala Asp Ala Gly His Ile Pro Ile Leu Leu Glu Ala Arg Asp Val Leu
66           130             135             140
68 ggt ggc aag gtg gca gcg tgg aaa gat gat gat gga gac tgg tat gag    482
69 Gly Gly Lys Val Ala Ala Trp Lys Asp Asp Asp Gly Asp Trp Tyr Glu
70      145             150             155
72 aca ggc ctg cat ata ttt ttt ggt gca tat ccc aat gtg cag aat tta    530
73 Thr Gly Leu His Ile Phe Phe Gly Ala Tyr Pro Asn Val Gln Asn Leu
74 160             165             170             175
76 ttt ggt gaa ctt ggc ata aat gat cgt cta caa tgg aaa gag cat tca    578
77 Phe Gly Glu Leu Gly Ile Asn Asp Arg Leu Gln Trp Lys Glu His Ser
78              180             185             190
80 atg att ttt gcg atg cca aac aag cca ggg gaa ttt agt cgc ttt gat    626
81 Met Ile Phe Ala Met Pro Asn Lys Pro Gly Glu Phe Ser Arg Phe Asp
82           195             200             205
84 ttt cca gaa gta ctt cct gct cca cta aat gga ata tgg gca atc ctt    674
85 Phe Pro Glu Val Leu Pro Ala Pro Leu Asn Gly Ile Trp Ala Ile Leu
86      210             215             220
88 aaa aac aat gaa atg ctc act tgg cca gag aaa gtg caa ttt gct att    722
89 Lys Asn Asn Glu Met Leu Thr Trp Pro Glu Lys Val Gln Phe Ala Ile
90      225             230             235
92 gga cta cta cct gca atg att ggg ggg cag cca tat gtt gaa gct cag    770
93 Gly Leu Leu Pro Ala Met Ile Gly Gly Gln Pro Tyr Val Glu Ala Gln
94 240             245             250             255
96 gat ggc tta aca gtt caa gag tgg atg aga aaa cag ggt gtg ccg gat    818
97 Asp Gly Leu Thr Val Gln Glu Trp Met Arg Lys Gln Gly Val Pro Asp
98              260             265             270
100 cga gtc aat gac gag gtt ttc att gca atg tca aag gct ctt aac ttc   866
101 Arg Val Asn Asp Glu Val Phe Ile Ala Met Ser Lys Ala Leu Asn Phe
102          275             280             285
104 ata aac cct gat gaa ctt tcc atg caa tgc atc ctg att gcc tta aac   914
105 Ile Asn Pro Asp Glu Leu Ser Met Gln Cys Ile Leu Ile Ala Leu Asn
106          290             295             300
108 cgt ttc ctt cag gaa aag cat ggg tcg aag atg gcc ttt tta gat ggt   962
109 Arg Phe Leu Gln Glu Lys His Gly Ser Lys Met Ala Phe Leu Asp Gly
110      305             310             315
112 aat cca cct gaa aga tta tgt aag cca att gct gat cac atc gag tca   1010
113 Asn Pro Pro Glu Arg Leu Cys Lys Pro Ile Ala Asp His Ile Glu Ser
114 320             325             330             335
116 ttg ggt ggc caa gtc atc ctt aat tcc cga ata cag aag att gag ctg   1058
117 Leu Gly Gly Gln Val Ile Leu Asn Ser Arg Ile Gln Lys Ile Glu Leu
118          340             345             350
120 aat gca gac aaa tcc gtc aag cat ttt gtg ctc acc aat gga aat ata   1106
121 Asn Ala Asp Lys Ser Val Lys His Phe Val Leu·Thr Asn Gly Asn Ile
122          355             360             365
124 ata aca gga gat gca tat gta ttt gca aca cct gtt gat atc ttg aag   1154
125 Ile Thr Gly Asp Ala Tyr Val Phe Ala Thr Pro Val Asp Ile Leu Lys
126          370             375             380
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128 ctt ctg tta cct gaa gat tgg aag gag att tca tat ttc aaa aaa ttg   1202
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132 gac aag ttg gtt ggc gta cct gtg ata aat gta cac ata tgg ttt gat   1250
133 Asp Lys Leu Val Gly Val Pro Val Ile Asn Val His Ile Trp Phe Asp
134 400                     405                 410                 415
136 agg aag ttg aag aac aca tac gat cat ctt ctt ttc agc agg agt cca   1298
137 Arg Lys Leu Lys Asn Thr Tyr Asp His Leu Leu Phe Ser Arg Ser Pro
138                     420                 425                 430
140 ctg ttg agc gtt tat gca gac atg tct gtt aca tgc aag gaa tac tac   1346
141 Leu Leu Ser Val Tyr Ala Asp Met Ser Val Thr Cys Lys Glu Tyr Tyr
142                 435                 440                 445
144 aat cca aat caa tcc atg ctt gag cta gta ttt gca cca gca gag aaa   1394
145 Asn Pro Asn Gln Ser Met Leu Glu Leu Val Phe Ala Pro Ala Glu Lys
146             450                 455                 460
148 tgg att tca tgc agt gac agt gaa atc att aac gcg act atg caa gag   1442
149 Trp Ile Ser Cys Ser Asp Ser Glu Ile Ile Asn Ala Thr Met Gln Glu
150     465                 470                 475
152 ctt gct aaa ctc ttt cca gat gag att tct gct gat caa agc aag gcc   1490
153 Leu Ala Lys Leu Phe Pro Asp Glu Ile Ser Ala Asp Gln Ser Lys Ala
154 480                 485                 490                 495
156 aaa att ttg aaa tat cat gtt gta aag acc ccg agg tca gtt tac aag   1538
157 Lys Ile Leu Lys Tyr His Val Val Lys Thr Pro Arg Ser Val Tyr Lys
158                 500                 505                 510
160 acg gtc cct gat tgt gaa cca tgc cgg cct ttg caa aga tct cca att   1586
161 Thr Val Pro Asp Cys Glu Pro Cys Arg Pro Leu Gln Arg Ser Pro Ile
162             515                 520                 525
164 gaa ggg ttc tac ttg gct ggt gac tac aca aag cag aag tat ttg gcc   1634
165 Glu Gly Phe Tyr Leu Ala Gly Asp Tyr Thr Lys Gln Lys Tyr Leu Ala
166             530                 535                 540
168 tca atg gaa ggt gcc gtg tta tct ggg aag cta tgt gct cag gca att   1682
169 Ser Met Glu Gly Ala Val Leu Ser Gly Lys Leu Cys Ala Gln Ala Ile
170     545                 550                 555
172 gtg cag gac tgc agc ttg ttg gct tct agg gta cag aaa agc cca cag   1730
173 Val Gln Asp Cys Ser Leu Leu Ala Ser Arg Val Gln Lys Ser Pro Gln
174 560                 565                 570                 575
176 acg ttg acg att gcc tga ttcaggaaac ttttatgcag gttcagtttg   1778
177 Thr Leu Thr Ile Ala
178                 580
180 taggggggaat atttctggtt ttgtttcatt cagatgtttt tcttttagag catatgtctt 1838
182 tatagtaaaa actcccacct ctttctcatg tatagctaca tcagcaagca aggggggtaa 1898
184 gttgcaattt caggacttga acatggcctc tgcacaggta aagacagaat ggacataaat 1958
186 gcaagcatgg aatttacaat attc   1982
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190 <211> LENGTH: 580
191 <212> TYPE: PRT
192 <213> ORGANISM: Hydrilla verticillata
194 <400> SEQUENCE: 2
195 Met Thr Val Ala Arg Ser Val Val Ala Val Asn Leu Ser Gly Ser Leu
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RAW SEQUENCE LISTING   DATE: 08/31/2006
PATENT APPLICATION: US/10/521,478A   TIME: 09:06:41

Input Set : N:\RJAVED\10521478.txt
Output Set: N:\CRF4\08312006\J521478A.raw

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200         35                  40                 45
201 Ala Phe Gly Ala Asn Ala Pro Tyr Ser Lys Ile Ala Ala Thr Lys Pro
202     50                  55                 60
203 Lys Pro Lys Leu Arg Pro Leu Lys Val Asn Cys Met Asp Phe Pro Arg
204 65                  70                  75                 80
205 Pro Asp Ile Asp Asn Thr Ala Asn Phe Leu Glu Ala Ala Ala Leu Ser
206             85                  90                 95
207 Ser Ser Phe Arg Asn Ser Ala Arg Pro Ser Lys Pro Leu Gln Val Val
208             100                 105                110
209 Ile Ala Gly Ala Gly Leu Ala Gly Leu Ser Thr Ala Lys Tyr Leu Ala
210         115                 120                 125
211 Asp Ala Gly His Ile Pro Ile Leu Leu Glu Ala Arg Asp Val Leu Gly
212     130                 135                 140
213 Gly Lys Val Ala Ala Trp Lys Asp Asp Asp Gly Asp Trp Tyr Glu Thr
214 145                 150                 155                160
215 Gly Leu His Ile Phe Phe Gly Ala Tyr Pro Asn Val Gln Asn Leu Phe
216             165                 170                175
217 Gly Glu Leu Gly Ile Asn Asp Arg Leu Gln Trp Lys Glu His Ser Met
218             180                 185                190
219 Ile Phe Ala Met Pro Asn Lys Pro Gly Glu Phe Ser Arg Phe Asp Phe
220         195                 200                205
221 Pro Glu Val Leu Pro Ala Pro Leu Asn Gly Ile Trp Ala Ile Leu Lys
222     210                 215                 220
223 Asn Asn Glu Met Leu Thr Trp Pro Glu Lys Val Gln Phe Ala Ile Gly
224 225                 230                 235                240
225 Leu Leu Pro Ala Met Ile Gly Gly Gln Pro Tyr Val Glu Ala Gln Asp
226             245                 250                255
227 Gly Leu Thr Val Gln Glu Trp Met Arg Lys Gln Gly Val Pro Asp Arg
228             260                 265                270
229 Val Asn Asp Glu Val Phe Ile Ala Met Ser Lys Ala Leu Asn Phe Ile
230         275                 280                 285
231 Asn Pro Asp Glu Leu Ser Met Gln Cys Ile Leu Ile Ala Leu Asn Arg
232     290                 295                 300
233 Phe Leu Gln Glu Lys His Gly Ser Lys Met Ala Phe Leu Asp Gly Asn
234 305                 310                 315                320
235 Pro Pro Glu Arg Leu Cys Lys Pro Ile Ala Asp His Ile Glu Ser Leu
236             325                 330                335
237 Gly Gly Gln Val Ile Leu Asn Ser Arg Ile Gln Lys Ile Glu Leu Asn
238             340                 345                350
239 Ala Asp Lys Ser Val Lys His Phe Val Leu Thr Asn Gly Asn Ile Ile
240         355                 360                 365
241 Thr Gly Asp Ala Tyr Val Phe Ala Thr Pro Val Asp Ile Leu Lys Leu
242     370                 375                 380
243 Leu Leu Pro Glu Asp Trp Lys Glu Ile Ser Tyr Phe Lys Lys Leu Asp
244 385                 390                 395                400
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245 Lys Leu Val Gly Val Pro Val Ile Asn Val His Ile Trp Phe Asp Arg
246             405             410             415
247 Lys Leu Lys Asn Thr Tyr Asp His Leu Leu Phe Ser Arg Ser Pro Leu
248             420             425             430
249 Leu Ser Val Tyr Ala Asp Met Ser Val Thr Cys Lys Glu Tyr Tyr Asn
250             435             440             445
251 Pro Asn Gln Ser Met Leu Glu Leu Val Phe Ala Pro Ala Glu Lys Trp
252         450             455             460
253 Ile Ser Cys Ser Asp Ser Glu Ile Ile Asn Ala Thr Met Gln Glu Leu
254 465             470             475                 480
255 Ala Lys Leu Phe Pro Asp Glu Ile Ser Ala Asp Gln Ser Lys Ala Lys
256             485             490             495
257 Ile Leu Lys Tyr His Val Val Lys Thr Pro Arg Ser Val Tyr Lys Thr
258             500             505             510
259 Val Pro Asp Cys Glu Pro Cys Arg Pro Leu Gln Arg Ser Pro Ile Glu
260         515             520             525
261 Gly Phe Tyr Leu Ala Gly Asp Tyr Thr Lys Gln Lys Tyr Leu Ala Ser
262         530             535             540
263 Met Glu Gly Ala Val Leu Ser Gly Lys Leu Cys Ala Gln Ala Ile Val
264 545             550             555                 560
265 Gln Asp Cys Ser Leu Leu Ala Ser Arg Val Gln Lys Ser Pro Gln Thr
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274 <212> TYPE: DNA
275 <213> ORGANISM: Glycine max
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278 <221> NAME/KEY: CDS
279 <222> LOCATION: (221)..(1933)
281 <400> SEQUENCE: 3
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286 tcttcagctc ttgttttttc ccaaatctac tttcaaagtg cctgaattct gcaacagtaa 180
288 tattaacact cctctctttt gttcaggctt tatttcccca atg gcc gct tgt ggc   235
289                                                Met Ala Ala Cys Gly
290                                                 1               5
292 tat ata tct gct gcc aac ttc aat tat ctc gtt ggc gcc aga aac ata   283
293 Tyr Ile Ser Ala Ala Asn Phe Asn Tyr Leu Val Gly Ala Arg Asn Ile
294             10              15              20
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300 agc gac tca atg ggt ctt act ttg cga ccc gct ccg att cgt gct cct   379
301 Ser Asp Ser Met Gly Leu Thr Leu Arg Pro Ala Pro Ile Arg Ala Pro
302         40              45              50
304 aag agg aac cat ttc tct ccc ttg cgt gtc gtt tgc gtc gat tat cca   427
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VERIFICATION SUMMARY   DATE: 08/31/2006
PATENT APPLICATION: **US/10/521,478A**   TIME: 09:06:42

Input Set : **N:\RJAVED\10521478.txt**
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L:15 M:270 C: Current Application Number differs, Replaced Application Number
L:16 M:271 C: Current Filing Date differs, Replaced Current Filing Date